

FIGURE 1

SEQ ID NO: 1

>STAAU_R009 nucleotide sequence: 1800
TTGCGAATAGATCAATCGATCATTAATGAAATAAAGATAAAAACCGACATTTAGACTTGGTAAGTGAATATGTAAATTTAGAAAAAGAG
AGGACGCAATATATAGGTTTGTCTCTTTTCATGATGAAAAGACACCTTCATTTACAGTTTCTGAAGATAAACAAATTTGTCAATTGTT
TTGGTTGTAAAAAGGTGGCAATGTTTTCAATTTACTCAAGAAATTAAGACATATCATTTGTTGAAGCGGTTAAAGAAATTAGGTGAT
AGAGTTAATGTTGCTGTAGATATTGAGGCAACACAATCTAACTCAAAATGTTCAAAATGCTGATGATTTACAAATGATTGAAATGCA
TGAGTTAATACAAAGAAATTTTATTATTACGCTTTAACAAAGACAGTCGAAGGCGAACAAGCATTTAAACGTACTTACAAGAACGTTGTTTA
CAGATCGCTTATTAAGAGCGGCGATTTGCTTTGACCCGATAGCTCACATTTTGTGTCATGATTTTCTTCAAAAAAAGGTTACGAT
ATTGAATTAGCATATGAAGCCGGATTATATCACGTAACGAAGAAAATTTTCAGTTATTACGATAGATTTTCGAAATCGTATTATGTTTCC
TTTGAAAAATGCGCAAGGAAGAAATGTTGGATATTTCAGGTCGAACATATACCGGTCAAGAACCAAAATACTTAAATAGTCTGAAACAC
CTATCTTTCAAAAAAGAAAGTTGTTATACAACTTAGATAAAGCGGTAAAATCAATTAGAAAAATTAGATGAAATCGTATTACTAGAAAGGT
TTTATGGATGTTATAAAATCTGATACTGCTGGCTTGAAAAACGTTGTTGCAACAATGGGTACACAGTTGTCAAGATGAACATATTACTTT
TATACGAAAGTTAACATCAAAATATAACATTAATGTTTGTGCGGATTTTGCAGGTAGTGAAGCAACACTTAAACAGGTCAAAAATTTGT
TACAGCAAGGGCTAAATGTATTTGTTATACAATTTGCCATCAGGCATGGATCCGGATGAATACATTTGTTAAGTATGGCAACGATGCATTT
ACTGCTTTTGTAAAAAATGACAAAAAGTCAATTTGCACATTATAAAGTGAGTATATTAAAAAGATGAAATTGACACATAATGACCTTTTCATA
TGAACGTTATTTGAAAGAACTAAGTCATGATATTTCGCTTATGAAATCATCGATTTTGCAACAAAAAGGCTTTAAATGATGTTGCACCAT
TTTTCAATGTTAGTCCTGAGCAATTAGCTAACGAAATACAATTCATCAAGCACCCAGCCAATTTATATCCAGAAGATGAGTATGGCGGT
TACATTGAACCTGAGCCAAATTTGGTATGGCACAATTTGACAATTTGAGCCGTCAAGAAAAAGCGGAGCGAGCATTTTAAAAACATTTAAT
GAGAGATAAGATACATTTTAAATTTATGAAAGTGTGATAAGGATAACTTCACAAATCAGCATTTTAAATATGTTATTCGAAGTCT
TACATGATTTTATGCGGAAAATGATCAATATAATATCAGTGTGCTGTGAGTATGTTAAATTCAAATGAGTTGAGAGAAAACACTAAT
AGCTTAGAACCAATATAAATTTGAATGACGAACCATATGAAAAATGAAATTTGATGATTATGTCAATGTTATTAAATGAAAAAGGACAAGAAAC
AATTGAGTCATTGAATCATAAATTAAGGGAAGCTACAAGGATTGGCGATGTAGAATTACAAAAATACTATTTACAGCAAAATTTGTTGCTA
AGAATAAAGAACCGCATGTAG

SEQ ID NO: 2

>STAAU_R009 amino acid sequence : 599
 LRIDQSIINEIKDKTDILDVSEYVKLEKGRNYIGLCPFHDEKTPSFTVSEDKQICHCFGCKKGGNVFQFTQEIKDISFVEAVKELGD
 RVNVAVDIEATQSNNSNVQIASDDLQMIEMHELIOEFYYALTKTVEGEQALTYLQERGETDALIKERGIGFAPDSSHCHDFLQKKGYD
 IELAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVGYSGRTYTGQEPKYLNSPETPIFQKRKLLYNLDKARKSIRKLDEIVLLEG
 FMDVIKSDTAGLKNVVATMGTLSDDEHITFIRKLTSNITLMFDGDFAGSEATLKTGQNLQQLNVFVIQLPSGMDPDEYIGKYGNDAF
 TAFVKNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKALNDVAPFFNVSPPEQLANEIQFNQAPANYYPEDEYGG
 YIEPEPIGMAQFDNLSRQEKAEAFILKHLMRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI
 SLEQYNLNDEPYENEIDDYVNVVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIVAKNKERM

FIGURE 2

SEQ ID NO: 3

>96ORF078 nucleotide sequence
 ATGAATATAATGCAATTCAAAAGCTTATTGAAATCGATGTATGAAGAGACAAAGCAAAGC
 GACCCGATTGTAGCAAAATGTATATCGAGACTGGTTGGCGGTCAATAGATTGTTGGAC
 AATAACGAGTTATCGCCTTTCGATGATTACGACAGAGTTGAAAAGAAAATCATGAATGAA
 ATCAACTGGAAGAAAACACACATTAAGGAGTGTAA

SEQ ID NO: 4

>96ORF078 amino acid sequence 96_NT|10148-10363|
 MNIMQFKSLLKSMYEETKQSDPIVANVYIETGWAVNRLLDNNELSPFDDYDRVEKKIMNE
 INWKKTHKEC

FIGURE 3

A.

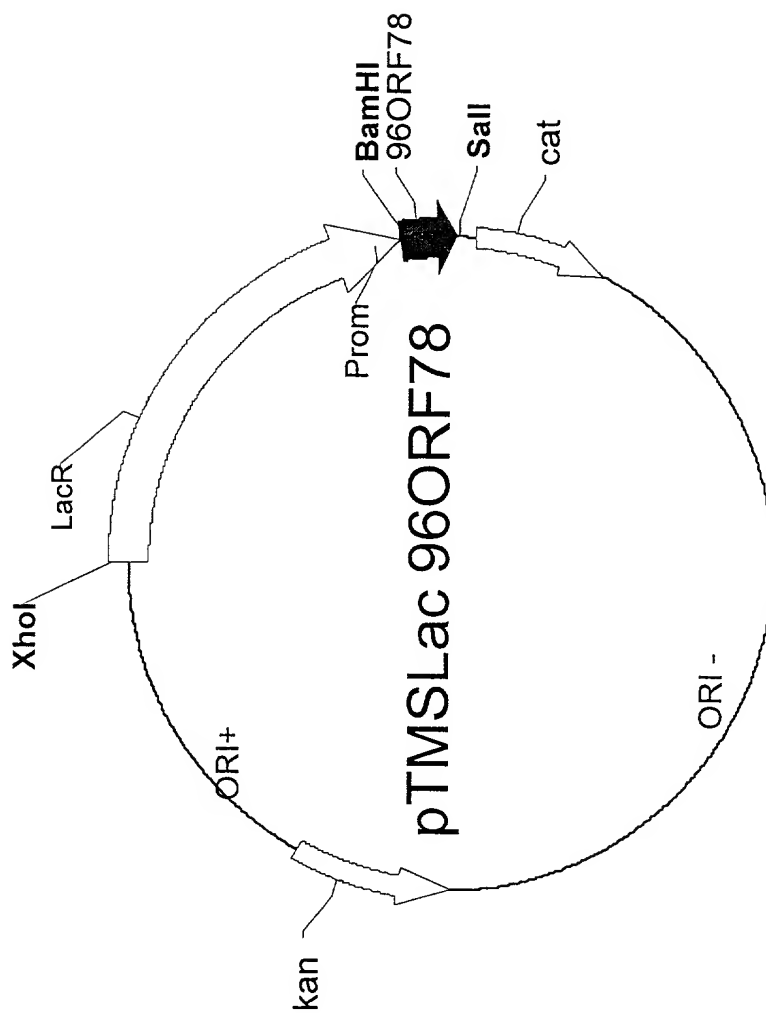


FIGURE 3 B.

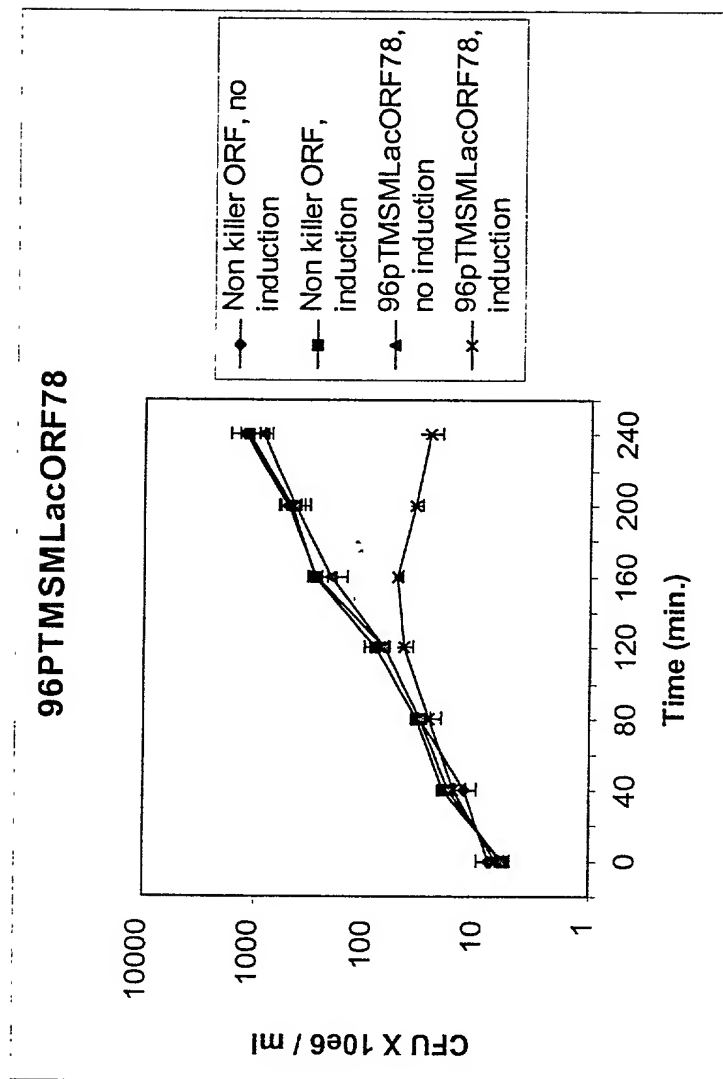
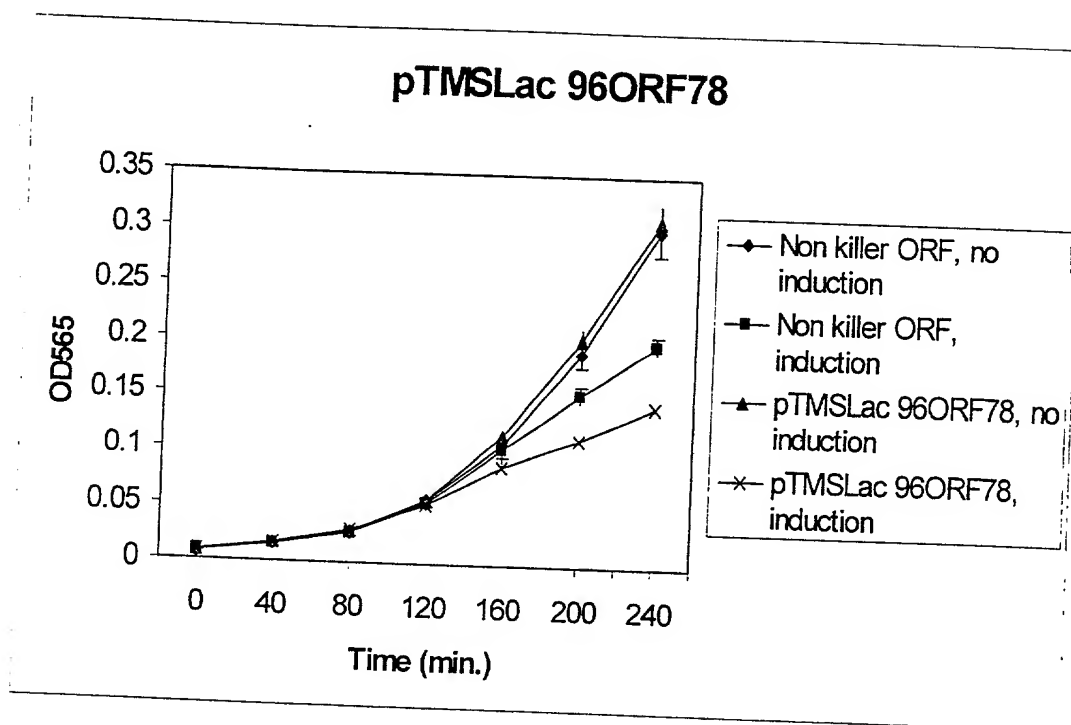


FIGURE 3 C.



D.

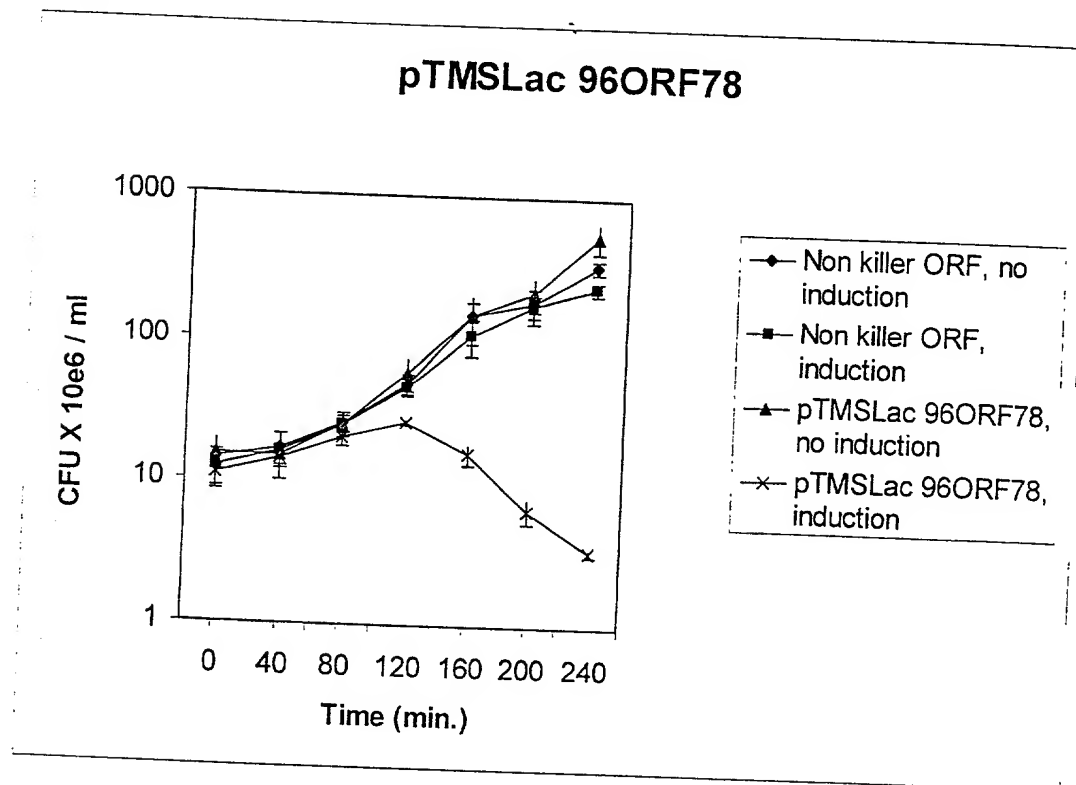


FIGURE 4

A. GST/96ORF78

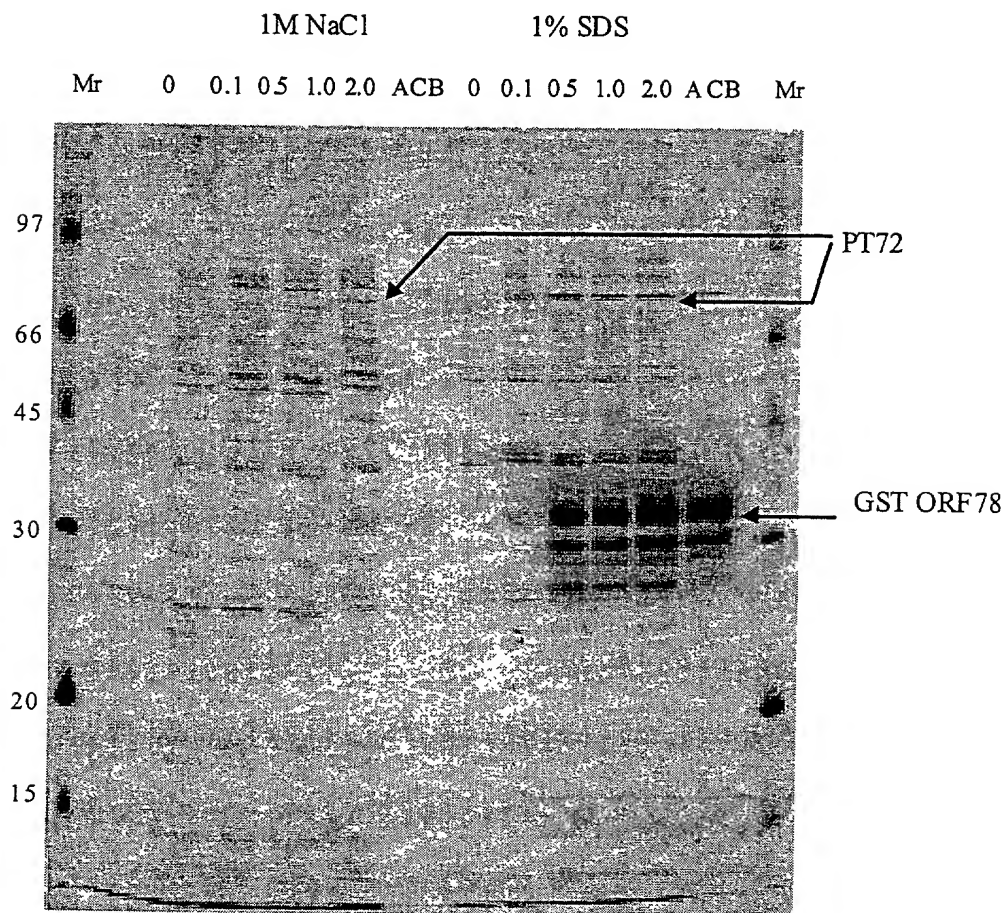


FIGURE 4

B. GST

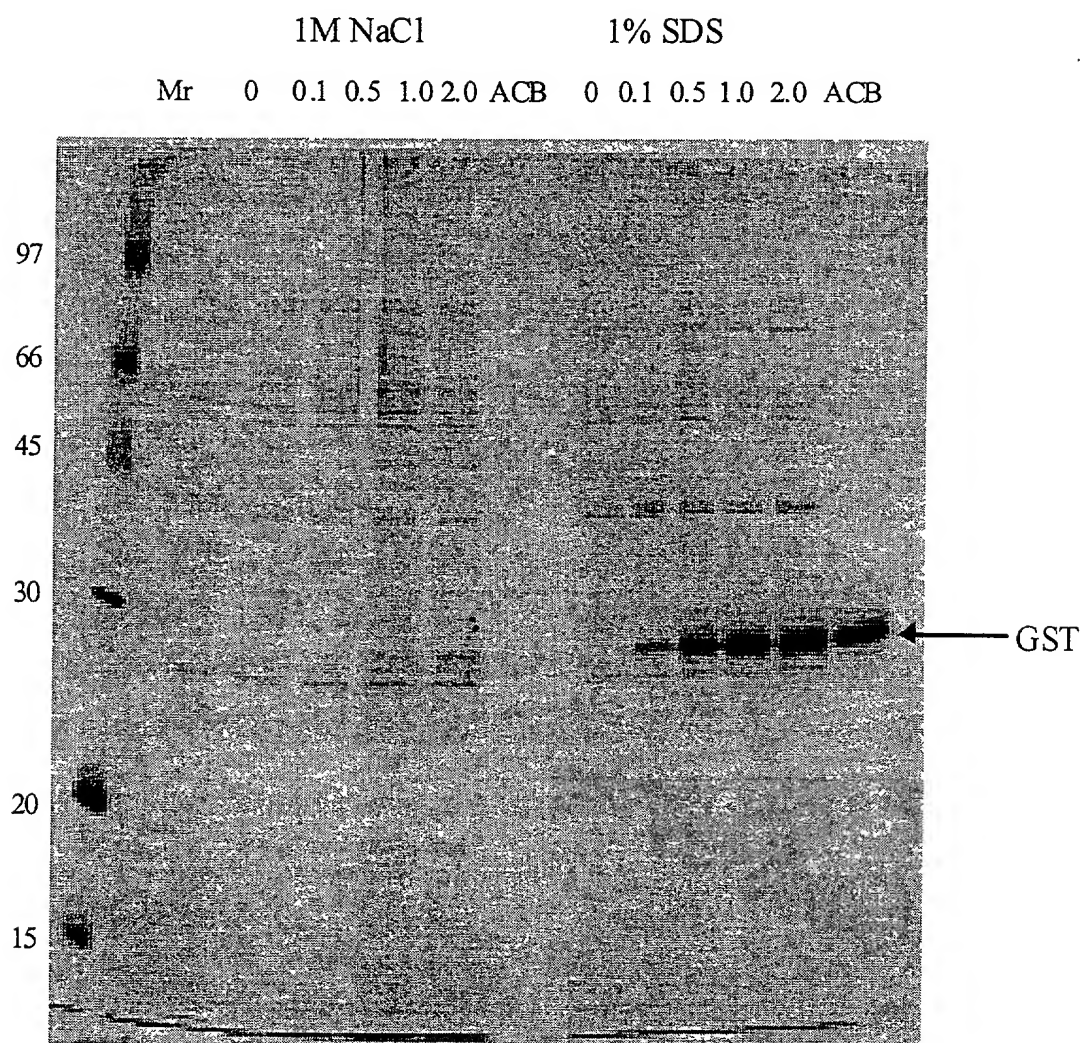


FIGURE 5 96ORF78 (GST removed)

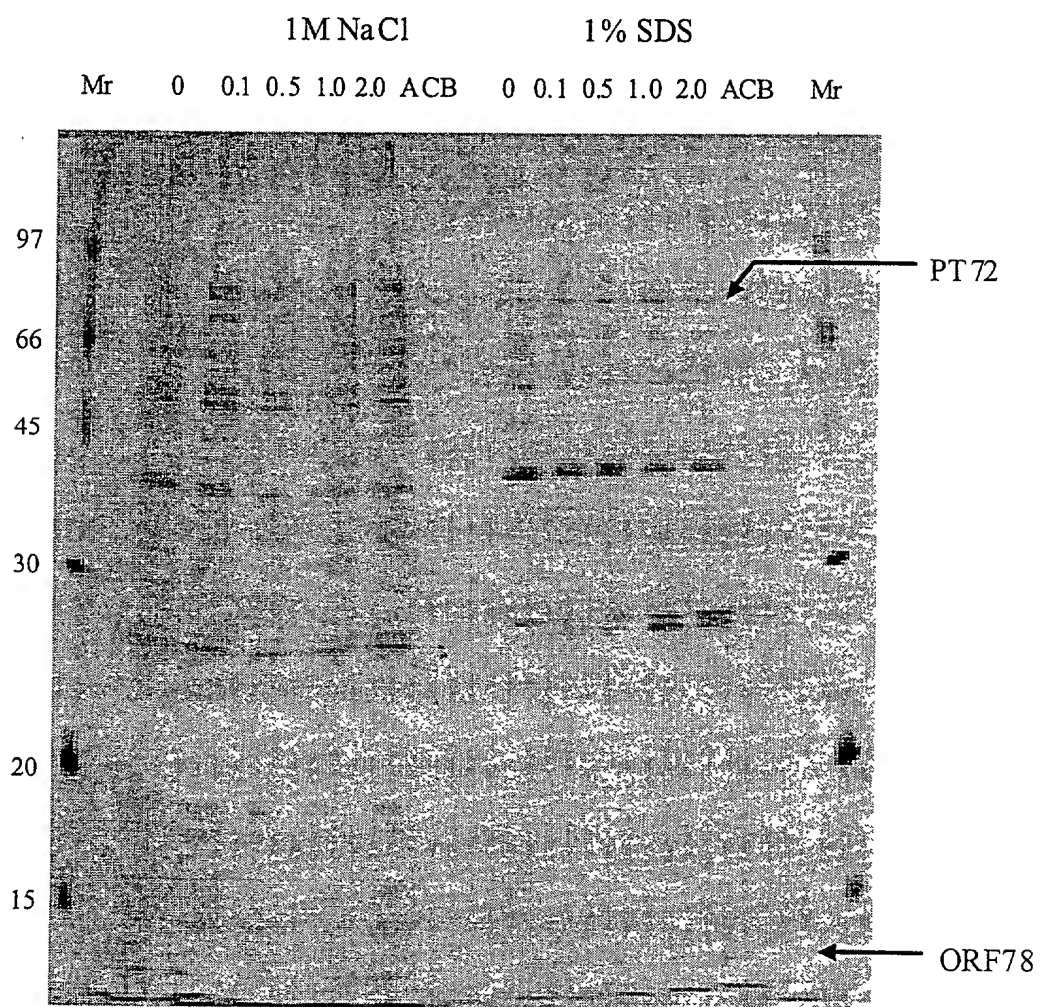
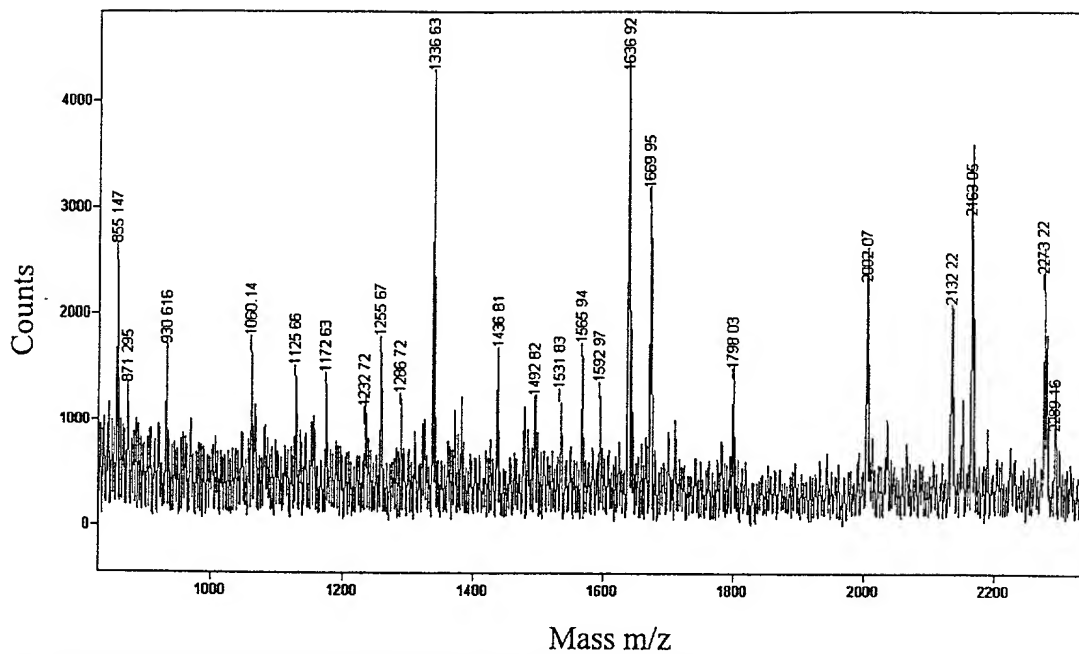


FIGURE 6



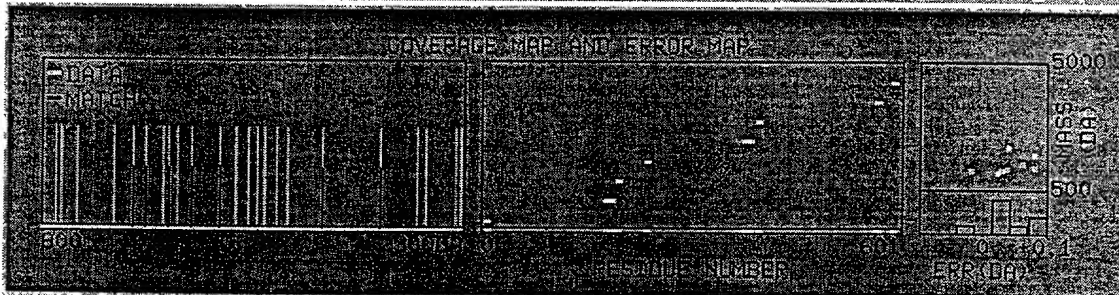
ouContig286: 82020 to 83822: Frame 3 601 aa

Sample ID: orf78.72 [Pass:0]

Measured peptides: 23

Matched peptides: 7

Min. sequence coverage: 14%



1124.649	M	1124.622	0.027	588	596	0	YYLQQIVAK
1171.623	M	1171.590	0.033	394	403	0	ELSHDISLMK
1171.623	M	1171.644	0.021	5	14	0	IDQSILNEIK
1254.661	M	1254.620	0.041	563	573	0	GQETIESLNHK
1335.627	M	1335.536	0.091	193	202	0	NEENFSYYDR
1435.802	M	1435.734	0.068	233	244	0	YLNSPETPIFOK
1797.019	M	1796.930	0.089	177	192	1	KGYDIELAYEAGLLSR
2001.060	M	2001.016	0.044	374	390	1	VSILKDEIAHNDLSYR

855.147 871.295 930.616 1060.140 1232.717 1286.716 1492.822 1531.830 1565.943 1592.967
1636.921 1669.948 2132.217 2163.048 2273.222 2289.164

FIGURE 7A

A. Pfam HMM search results

Model	Seq-from	Seq-to	HMM-from	HMM-to	Score	E-value
zf-CHC2	3	100	1	98	198.4	1.1e-55
Toprim	260	339	1	151	71.9	1.3e-17

Alignments of top-scoring domains:

zf-CHC2:
domain 1 of 1, from 3 to 100: score 198.4, E = 1.1e-55
*->ipeesIdelknriDIVdvisYVklkKkGrnYkgLCPFFHdEKTPSFs
i++++I+e+k+++DI d++seYVkl+K+GrnY+gLCPFFHdEKTPSF+
gi|133988 3 IDQSIINEIKDKTDILDVSEYVklEKRGRNYIGLCPFFHdEKTPSFT 49

VspeKqfYhCFGCGagGdaIkFlmkyeklsFvEAvekLAdragidlpyek
Vs +Kq+ hCFGc++g+++ F ++++++sFvEAv++L dr+++ +++e
gi|133988 50 VSEDKQICHCFGCKKGGNVFQFTQEIKDIFVEAVKELGDRVNVAVDIEA 99

g<-*
+
gi|133988 100 T 100

Toprim: domain 1 of 1, from 260 to 339: score 71.9, E = 1.3e-17

```

*->kvliiVEgpsdakalakalgpkskrkivyelpggkdgnavvaslGhlv
+++++ Eg++d+++ a+ +nvva++G+
gi|133988 260 DEIVLLEGFMDVIKSDTAGL-----KNVVATMGQTQ- 289

dLptpegyddykwllwlpivdvkkgfepyqiefdqlckcskkidlkkeql
+++++
gi|133988 290 -----LSDEHI 295

kllkklakadevilatDpDreGeaiawkllellkpygpveleddkkvrr
++kl+++ + l++D+D +G ++++k + l+ +g +v++
gi|133988 296 TFIRKLTSN---ITLMFDGDFAGSEATLKTGQNLLQQGL-----NVFV 335

iflp<-*
i+lp
gi|133988 336 IQLP 339

```

FIGURE 7B

B. Optimal global alignment of amino acid sequences

Sequence 1 sp|O05338|PRIM_STAAU_DNA_PRIMASE (EC 2.7.7.-) - S. aureus. (572 letters)
Sequence 2 STAAU_R009 STAAU_R009 NT|1-1800| (599 letters)

Identical: 560/605 (92%), Similar: 564/605 (93%), Gap: 39/605 (6%)

seq1	1	M-----	-----IGLCPFHDEKTPSFTVSEDKQICHCF	27
seq2	1	LRIDQSIINEIKDKTDILDVSEYVKLEKGRNYIGLCPFHDEKTPSFTVSEDKQICHCF		60
seq1	28	GCKKGGNVFQFTQEI	KDISFVEAVKELGDRVNVAVDIEATQSNSNVQIASDDLQMIEMHE	87
seq2	61	GCKKGGNVFQFTQEI	KDISFVEAVKELGDRVNVAVDIEATQSNSNVQIASDDLQMIEMHE	120
seq1	88	LIQEFYYALT	KTVEGEQALTYLQERGETDALIKERGIGFAPDSSHFCHDFLQKKGYDIE	147
seq2	121	LIQEFYYALT	KTVEGEQALTYLQERGETDALIKERGIGFAPDSSHFCHDFLQKKGYDIE	180
seq1	148	LAYEAGLLSRNEENFSY	DRFRNRIMFPLKNAQGRIVYSGRTYTGQEPKYLNSPETPIF	207
seq2	181	LAYEAGLLSRNEENFSY	DRFRNRIMFPLKNAQGRIVYSGRTYTGQEPKYLNSPETPIF	240
seq1	208	QKRKLLYNLDKARKSIR	KLDEIVLLEGFMDVIKSDTAGLKNVVATMGTLQSDHEHITFIRK	267
seq2	241	QKRKLLYNLDKARKSIR	KLDEIVLLEGFMDVIKSDTAGLKNVVATMGTLQSDHEHITFIRK	300
seq1	268	LTSNITLMFDGDFAGSE	ATLKTGQHLLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTTFV	327
seq2	301	LTSNITLMFDGDFAGSE	ATLKTGQNLQQGLNVFVIQLPSGMDPDEYIGKYGNDAFTAFV	360

Table 2

seq1	328	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKAINDVAPFFNVS	387
seq2	361	KNDKKSFAHYKVSILKDEIAHNDLSYERYLKELSHDISLMKSSILQQKALNDVAPFFNVS	420
seq1	388	PEQLANEIQFNQAPANYYPEDEYGGYDEYGGYIEPEPIGMAQFDNLSRREKAERAFKLHL	447
seq2	421	PEQLANEIQFNQAPANYYPE-----DEYGGYIEPEPIGMAQFDNLSRQEKAEARAFKLHL	474
seq1	448	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI	507
seq2	475	MRDKDTFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQYNISDAVQYVNSNELRETLI	534
seq1	508	SLEQYNLNGEPYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQYYLQQIVAK	567
seq2	535	SLEQYNLNDEPYENEIDDYVNVINEKGQETIESLNHKLREATRIGDVELQYYLQQIVAK	594
seq1	568	NKERM	572
seq2	595	NKERM	599

Sequence 1 STAAU_R009 (599 letters)
Sequence 2 gi19910841|sp|Q9X4D0|PRIM_BACST DNA PRIMASE(597 letters)

Identical: 209/609 (34%), Similar: 315/609 (51%), Gap: 22/609 (3%)

seq1	1 L--RIDQSIINEIKDKTDILDVSEYVVKLEKGRNYIGLCPFHDEKTPSFTVSEDKQICH	58
	: : : : : : : :	
seq2	1 MGHRIPEETIEAIRRGVDIVDVIGEYVQLKRQGRNYFGLCPFHGEKTPSFSVPEKQIFH	60
seq1	59 CFGCKKGGNVFQFTQEIKDISFVEAVKELGDRNVNAVVDIEATQNSNNVQIASDDLQ-MIE	117
	: : : : : :	
seq2	61 CFGCGAGGNAFTFLMDIEGIPFVEAAKRLAAKAGVDLSVYELDVGRDDGQTDEAKAMTE	120
seq1	118 MHELIQEFYYALTKTVEGEQALTYLQERGFTDALIKERGIGFAPDSSHFDLQKKGY	177
	: : :	
seq2	121 AHALLKRFYHLLVHTKEGQAALDYLAQARGWTKETIDRFEIGYAPDAPDAAAKLLESHSF	180
seq1	178 DIELAYEAGLLSRNEENFSYYDRFRNRIMFPLKNAQGRIVYSGRTYTGQEPKYLNSPET	237
	: : : : : :	
seq2	181 SLPVMEKAGLLTKKEDG-RYVGRFRNRIMFPIHHRGETVGFSGRLLGEGHPKYVNSPET	239
seq1	238 PIFQKRKLLYNLDKARKSIRKLDLDEIVLLEGFMDVIKSDTAGLKNVVATMGTLSDHEHITF	297
	: : : : :	
seq2	240 PVFRKGAILYHFHAARVPIRKRQEALLVEGFADVISAAQAGIDYAIATMGTSLTEEQARI	299
seq1	298 IRKLTSNITLMFDGDFAGSEATLKTGQNLQGLNVFVIQLPSGMDPDEYIGKYGNDAFT	357
	: : :	
seq2	300 LRP-CDTITICYDGDRAIEAAWAAAEQLSALGCRVKVASLPNGLDPDEYIRVYGGGERF-	357
seq1	358 AFVKNDKKSFAYHKVSIKDEIAHNDLSY-----RYLKELSHDISLMKSSILQQKALNDV	413
	: : : : : : : :	
seq2	358 AGEAGCRRPLVAFKMAYLR--RGKNLQHEGERLRYIDEALREIGKLSSPVEQDYLRQL	414

Table 2. Sequence

seq1	414	APFFNVSPEQLANEIQFNQAPANYYPEDEYGGYIEPEPIGMAQFDNLSRQEKAERAF LKH	473
		: : :	
seq2	415	AEFSLSLSALHEQLSRQERTKPREAPDGETARP----MLAKKLLPAFQNAERLLLAH	470
seq1	474	LMRDKDTFLNYYESVDKDNFTNQHFYVFEVLHDFYAENDQYNISDAVQYVNSNELRETL	533
		: : : : : : : : :	
seq2	471	MMRSRDVALVVQERIG-GRFNIEEHRALAAAYIYAFYEEGHEADPGALISRI-PGELQPLA	528
seq1	534	ISLEQYNLNDEPYENEIDDDYV-NVINEKGQETIESLNHKLREATRIGDVELQKYYLQQIV	592
		: : : : : : : : : : :	
seq2	529	SDVSLLLIADDVSEQELEDYIRHVLNRPKWLMLKVKEQKTEAERRKDFLTAARIAKEMI	588
seq1	593	AKNK--ERM	599
seq2	589	EMKKMLSSS	597

[illegible]

10

58

160

118

119

178

175

235

234

295

1

767

SECRET

7CC

354

44

112

275

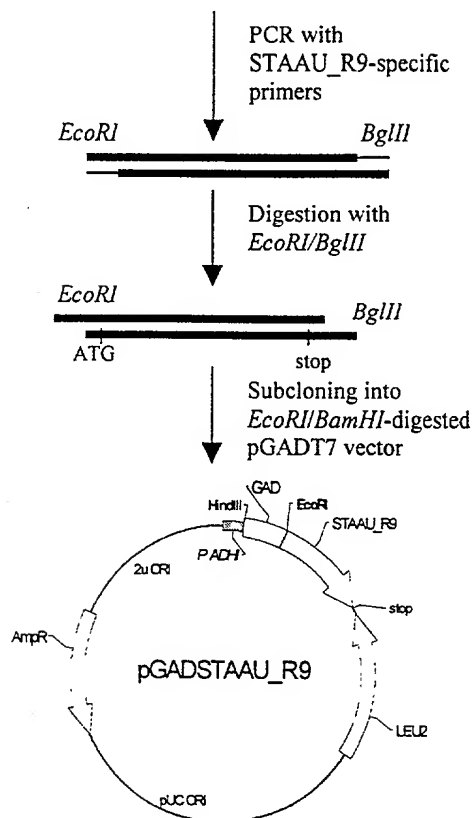
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Table 2

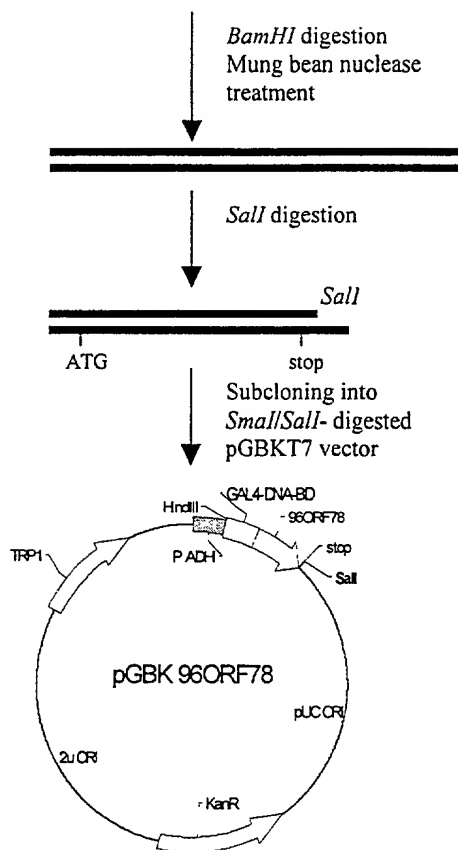
seq1	413	VAPFFNVSP	EQLANEIQF--NQAPANYYP	DEYGGYIEPEPIGMAQFDNLSRQ	KAERAF	470
seq2	407	LRIYLR---	QELGNKLGILDDSQ	LERLMPKAAESG	VS	454
seq1	471	LKHLMRDKD--	TFLNYYESVDKDNFTNQHFKYVFEVLHDFYAENDQY	NISDAVQYVNSNE		528
seq2	455	IGLLVQNPELATLVP	PLENLDENKLPGLG---LFREL	VNTCLS	QPG	511
seq1	529	LRETLISLEQY-----	NLNDEPYENEIDDDYVNVINEKGQETIESLNHKL	REATR--IGD		580
seq2	512	NAATLEKLSMWDDIADKNIAEQ	FTDSL	NHMFDS	LLELRQEELIA-----RERTHGLSNE	566
seq1	581	VELQYYYLQ	QIVAKNKERM		599	
seq2	567	ERLELWTLNQ	ELAKK----		581	

FIGURE 8

A- *Staphylococcus aureus* genomic DNA



B- 96pTMSMLacORF78



C-

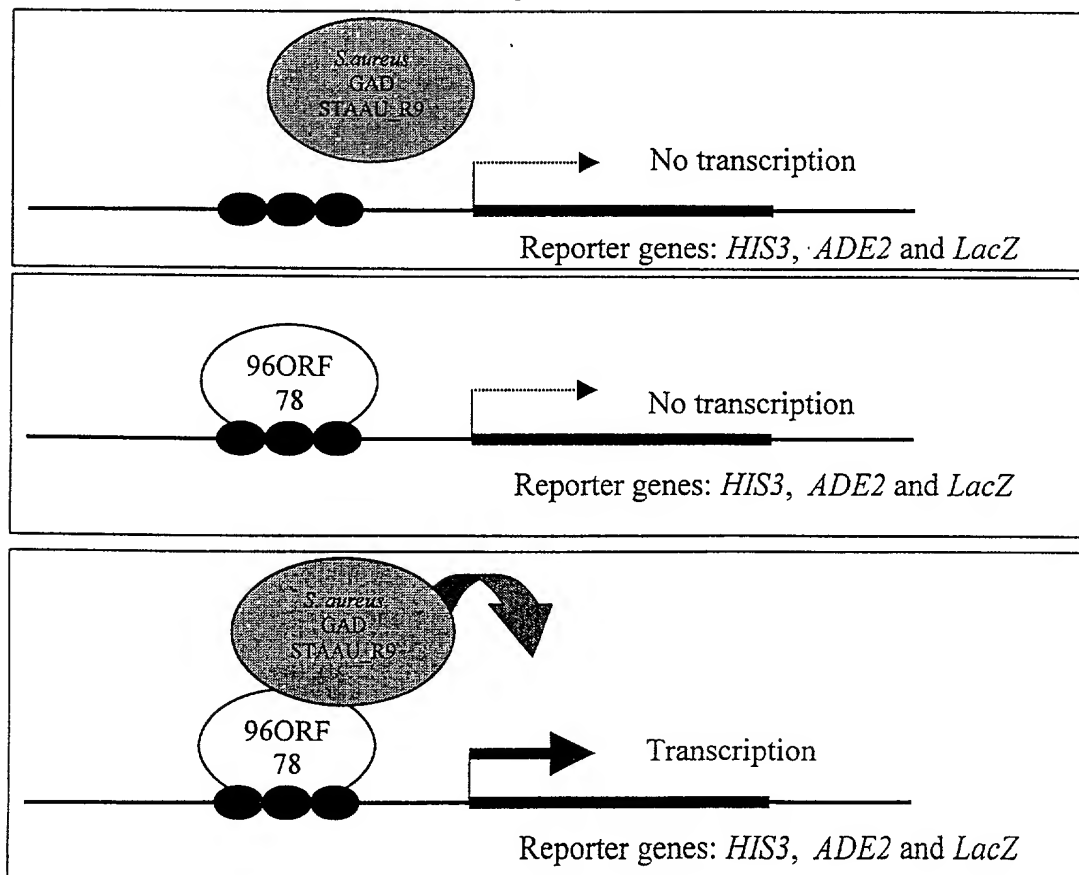
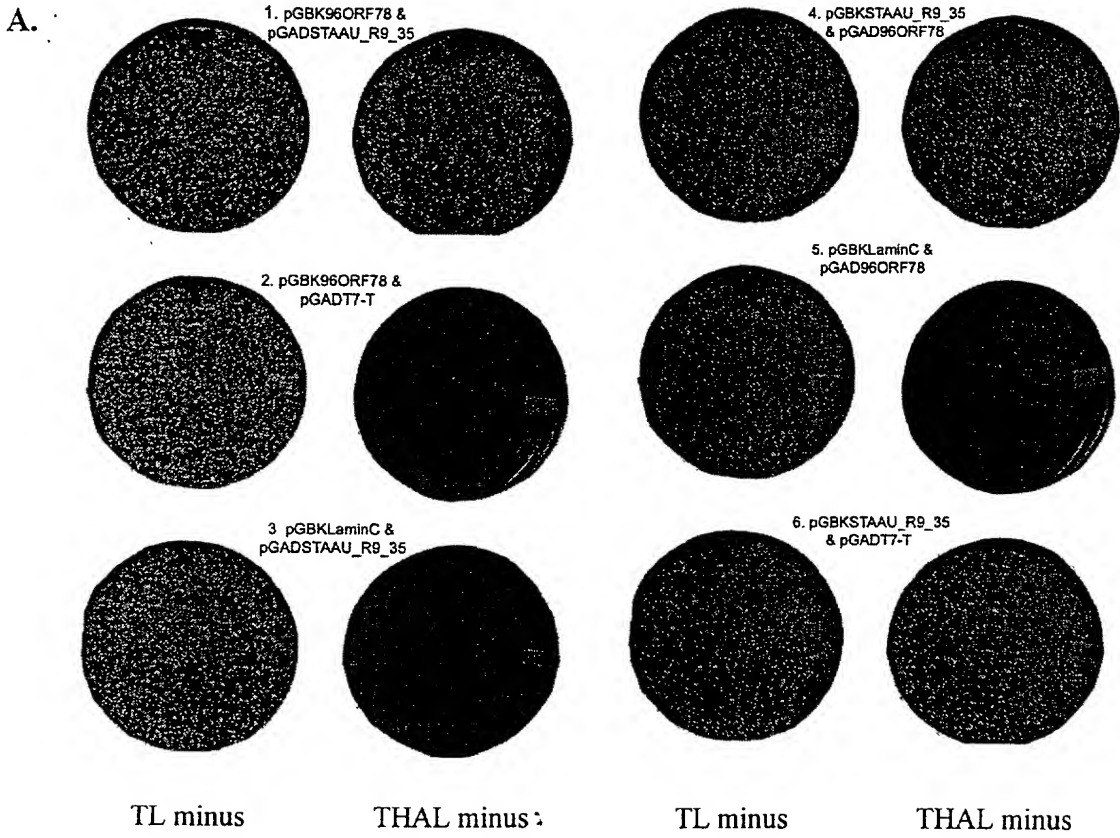
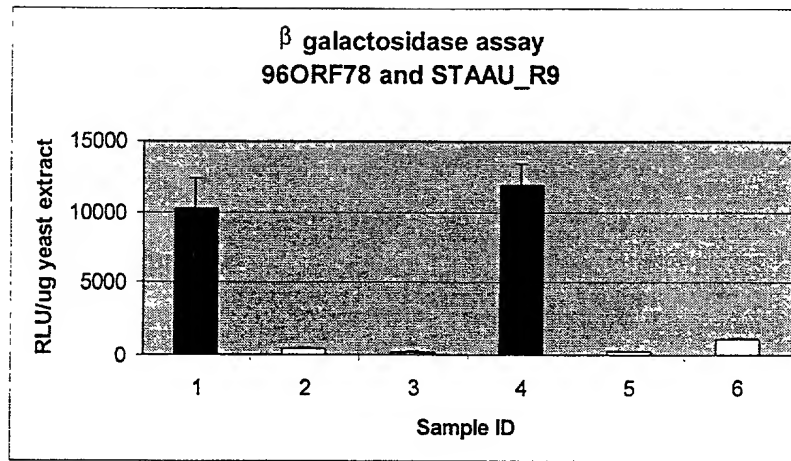


FIGURE 9



B.



Sample	Yeast co-transformants		RLU (avg)	SD
	Plasmid 1	Plasmid 2		
1	pGBK 96ORF78	pGADSTAAU_R9_35	10, 250	2, 080
2	pGBK 96ORF78	pGADT7-T	475	38
3	pGBK Lamin C	pGADSTAAU_R9_35	224	10
4	pGBKSTAAU_R9_35	pGAD 96ORF78	11, 935	1, 477
5	pGBK Lamin C	pGAD 96ORF78	243	12
6	pGBKSTAAU_R9_35	pGADT7-T	1, 121	37

FIGURE 10

A. Fragments of STAAU_R9

B.

Interaction with
96ORF78

1	599	Yes
35	599	Yes
35	342	No
229	402	No
229	599	Yes
380	599	Yes
380	449	No
380	490	No
380	530	No
380	561	No
449	599	Yes
490	599	Yes
530	599	Yes
561	599	Yes

SEQ ID NO: 6 STAAU_R9_561-599
AMINO ACID SEQUENCE

GQETIESLNHKLREATRIGDVELQKYLYLQQIVAKNKERM

SEQ ID NO: 5 STAAU_R9_1683-1800
NUCLEIC ACID SEQUENCE

GGACAAAGAAACAATTGAGTCATTGAATCATAAATTAAGGGAAGCTACAAGGATTGGCGATGTA
GAATTACAAAATACTATTACAGCAAAATTGTTGCTAAGAATAAAGAACGCATGTAG

C.

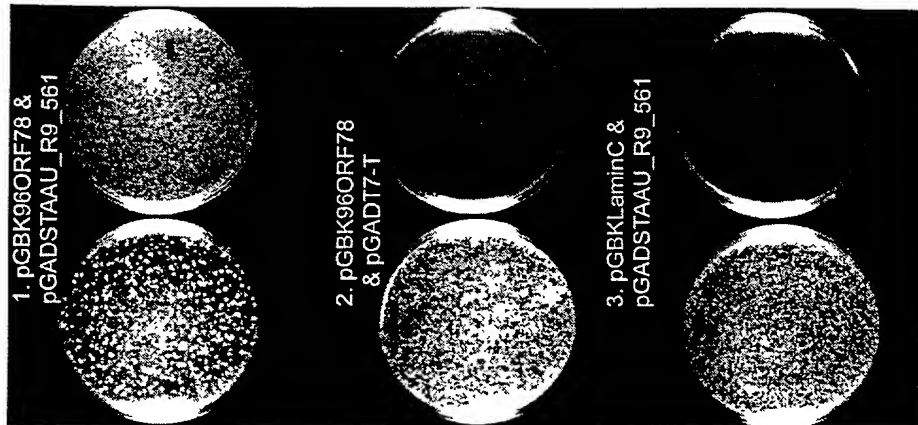


FIGURE 11

	Primer name	Primer sequence	Restriction site
SEQ ID NO: 8	R9_5E3	5'-ccggaattcTTGCGAATAGATCAATCG-3'	EcoRI
SEQ ID NO: 9	R9_3BG	5'-ggaagatctCTACATGCGTTCITTAATC-3'	BglII
SEQ ID NO: 10	R9_5E	5'-ccggaattcATGATAGGTTTGTGTCCT-3'	EcoRI
SEQ ID NO: 11	R9_5E1	5'-ccggaattcCCAAAATACCTAAATAGTCC-3'	EcoRI
SEQ ID NO: 12	R9_5E2	5'-ccggaattcGCACATAATGACCTTTCA-3'	EcoRI
SEQ ID NO: 13	R9_342R	5'-cgcggatccATGCCTGATGGCAATTG-3'	BamHI
SEQ ID NO: 14	R9_402R	5'-ccatcgatGATTTTCATAAGCGAAATATC-3'	Clal
SEQ ID NO: 15	R9_449F	5'-ccggaattcCTGAGCCAATTGGTATGGC-3'	EcoRI
SEQ ID NO: 16	R9_449R	5'-cgcggatccctaAGGTTCAATGTAACCGCC-3'	BamHI
SEQ ID NO: 17	R9_490F	5'-ccggaattcAAGGATAACTTCACAAATCAG-3'	EcoRI
SEQ ID NO: 18	R9_490R	5'-cgcggatccctaCTTATCAACACTTTCATAATA-3'	BamHI
SEQ ID NO: 19	R9_530F	5'-ccggaattcAGAGAAACACTAATTAGCTTA-3'	EcoRI
SEQ ID NO: 20	R9_530R	5'-cgcggatccctaTCTCAACTCATTTGAATTAAC-3'	BamHI
SEQ ID NO: 21	R9_561F	5'-ccggaattcGGACAAGAAACAATTGAGTC-3'	EcoRI
SEQ ID NO: 7	R9_561R	5'-cgcggatccctaTCCTTTTTCATTAATAACATTG-3'	BamHI

A.

B.

Cloning of SEQ ID NO: 2 amino acid fragments	Sense primer	Antisense primer
1-599	R9_5E3	R9_3BG
35-599	R9_5E	R9_3BG
35-342	R9_5E	R9_342R
229-402	R9_5E1	R9_402R
229-599	R9_5E1	R9_3BG
380-599	R9_5E2	R9_3BG
380-449	R9_5E2	R9_449R
380-490	R9_5E2	R9_490R
380-530	R9_5E2	R9_530R
380-561	R9_5E2	R9_561R
449-599	R9_449F	R9_3BG
490-599	R9_490F	R9_3BG
530-599	R9_530F	R9_3BG
561-599	R9_561F	R9_3BG